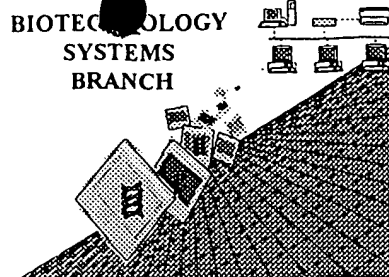


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/833,031  
Source: OIPÉ  
Date Processed by STIC: 08/06/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/833,031
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 _____ Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <del>_____</del> Use of n's or Xaa's (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 _____ Invalid <213> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 _____ Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,031

DATE: 08/06/2001

TIME: 15:32:37

Input Set : A:\Gilad2b1.app

Output Set: N:\CRF3\08062001\I833031.raw

3 <110> APPLICANT: GILAD, Shlomit  
 4 EINAT, Paz  
 5 GROSMAN, Avital  
 7 <120> TITLE OF INVENTION: METHOD FOR ENRICHMENT OF NATURAL ANTISENSE MESSENGER  
 8 RNA  
 10 <130> FILE REFERENCE: GILAD=2B  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/833,031  
 C--> 13 <141> CURRENT FILING DATE: 2001-04-11  
 15 <150> PRIOR APPLICATION NUMBER: 09/680,420  
 16 <151> PRIOR FILING DATE: 2000-10-06  
 18 <160> NUMBER OF SEQ ID NOS: 29  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 2 <210> SEQ ID NO: 1  
 3 <211> LENGTH: 40  
 4 <212> TYPE: DNA  
 15 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: n at position 40 represents g, a, c or t  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: OLIGONUCLEOTIDE  
 32 PRIMERS  
 34 <400> SEQUENCE: 1  
 W--> 35 ttctagaatt cagcgccgc tttttttttt ttttttttv  
 38 <210> SEQ ID NO: 2  
 39 <211> LENGTH: 22  
 40 <212> TYPE: DNA  
 41 <213> ORGANISM: Artificial Sequence  
 43 <220> FEATURE:  
 44 <223> OTHER INFORMATION: Description of Artificial Sequence: OLIGONUCLEOTIDE  
 45 PRIMERS  
 47 <400> SEQUENCE: 2  
 48 gatgggagtt gtgtgttttag tc  
 51 <210> SEQ ID NO: 3  
 52 <211> LENGTH: 22  
 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Artificial Sequence  
 56 <220> FEATURE:  
 57 <223> OTHER INFORMATION: Description of Artificial Sequence: OLIGONUCLEOTIDE  
 58 PRIMERS  
 60 <400> SEQUENCE: 3  
 61 ggagagagaa gtgcagagtt cg  
 64 <210> SEQ ID NO: 4  
 65 <211> LENGTH: 21  
 66 <212> TYPE: DNA  
 67 <213> ORGANISM: Artificial Sequence  
 69 <220> FEATURE:  
 70 <223> OTHER INFORMATION: Description of Artificial Sequence: OLIGONUCLEOTIDE

Does Not Comply  
 Corrected Diskette Needed  
 PP. 3-5

OLIGONUCLEOTIDE  
 OLIGONUCLEOTIDE  
 40

22

22

## RAW SEQUENCE LISTING

DATE: 08/06/2001

PATENT APPLICATION: US/09/833,031

TIME: 15:32:37

Input Set : A:\Gilad2b1.app

Output Set: N:\CRF3\08062001\I833031.raw

```

71      PRIMERS
73 <400> SEQUENCE: 4
74 ttagtacaaa cttagggctc t                                21
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 20
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
84      PRIMERS
86 <400> SEQUENCE: 5
87 tcatggcaac tccagagcag                                20
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 20
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
97      PRIMERS
99 <400> SEQUENCE: 6
100 accacagtcc atgccatcac                                20
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
110      PRIMERS
112 <400> SEQUENCE: 7
113 tccaccaccc tgttgctgta                                20
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 22
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
123      PRIMERS
125 <400> SEQUENCE: 8
126 ggagttagtc cttgaccact ag                                22
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence:OLIGONUCLEOTIDE
136      PRIMERS
138 <400> SEQUENCE: 9
139 gcacttacac agttagtcac gg                                22
142 <210> SEQ ID NO: 10

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/833,031

DATE: 08/06/2001  
TIME: 15:32:37

Input Set : A:\Gilad2b1.app  
Output Set: N:\CRF3\08062001\I833031.raw

143 <211> LENGTH: 188  
144 <212> TYPE: DNA  
145 <213> ORGANISM: Artificial Sequence  
147 <220> FEATURE:  
148 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED  
149 SEQUENCE  
151 <400> SEQUENCE: 10  
152 gggcgggccc cttttttttt tttttttttg gagttagtcc ttgaccacta gtttgatgcc 60  
153 atctccattt tgggtgacct gtttcaccag caggcctgtt actctccatg actaactgtg 120  
154 taagtgttta aaatggaata aattgctttt ctacataacc ccaaaaaaaaa aaaaaaaaaa 180  
155 gcggccgc 188  
158 <210> SEQ ID NO: 11  
159 <211> LENGTH: 169  
160 <212> TYPE: DNA  
161 <213> ORGANISM: Artificial Sequence  
163 <220> FEATURE:  
164 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED  
165 HUMAN  
167 <400> SEQUENCE: 11  
168 tttttttttt ttttttttgg agttagtcct tgaccactag tttgatgcc tctccatttt 60  
169 ggggtgacctg tttcaccagc aggcctgtta ctctccatga ctaactgtgt aagtgtctaa 120  
170 aatggaataa attgcttttc tacataacc ccaaaaaaaaa aaaaaaaaaa 169  
173 <210> SEQ ID NO: 12  
174 <211> LENGTH: 550  
175 <212> TYPE: DNA  
176 <213> ORGANISM: Artificial Sequence  
178 <220> FEATURE:  
179 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED  
180 HUMAN  
182 <220> FEATURE: *not enumerated*  
183 <223> OTHER INFORMATION: n at positions 114, 319, 340, 350, 369, 386, 455,  
184 371, 506, and 538 are unknown. *Field 221*  
186 <400> SEQUENCE: 12  
187 ttttcattgt cataattttt tattatgtat caaattgtct tcaatataag ttacaacttg 60  
W--> 188 attaaagttg atagacattt gtatctattt aaagacaaaa aaattctttt atgthcaata 120  
189 tcttgtctag agtctagcaa atatagtacc tttcattgca ggatttctgc ttaatataac 180  
W--> 190 aagcaaaanc aaacaactga aaaaatataa accaaagcaa accaaacccc ccgtcact 240  
191 acaaatgtca atattgaatg aagcattaaa agacaacat aaagtaactt cagcttttat 300  
W--> 192 ctatgaatgc agaattgaatn ctaaaattag nggcaaaaaa ncaaacaaca aacaacaaac 360  
W--> 193 aaaacaaanc aaacaancaa aaaatcccac caatcttcat gggtaaactt tctgtctcag 420  
W--> 194 ggatgtaagc tgaactctaga ccattgccc ttctgtcgga tagcacagcc angatcact 480  
W--> 195 gaagatcatg ccaaatntca tgaccacggc aatgccgatg cccctgcgcc gatgatgg 540  
196 aatttattgg 550  
199 <210> SEQ ID NO: 13  
200 <211> LENGTH: 491  
201 <212> TYPE: DNA  
202 <213> ORGANISM: Artificial Sequence  
204 <220> FEATURE:  
205 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED

*position 189 not declared*  
*position 350 not enumerated*  
*position 377 not enumerated*  
*446 not enumerated*  
*position 196 not enumerated*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 08/06/2001

PATENT APPLICATION: US/09/833,031

TIME: 15:32:37

Input Set : A:\Gilad2b1.app

Output Set: N:\CRF3\08062001\I833031.raw

206 HUMAN

208 &lt;400&gt; SEQUENCE: 13

```

209 tttttttttt tttttttctt gctgcagcaa cgcgagtggg agcaccagga tctcgggctc 60
210 ggaacgagac tgcacggatt gttttaagaa aatggcagac aaaccagaca tgggggaaat 120
211 cgccagcttc gataaggcca agctgaagaa aacggagacg caggagaaga acaccctgcc 180
212 gaccaaagag accattgagc aggagaagcg gagtgaattt tcctaagatc ctggaggatt 240
213 tcctaccccc atcctcttcg agaccccgat cgtgatgtgg aggaagagcc acctgcaaga 300
214 tggacacgag ccacaagctg cactgtgaac ctgggcaact cgtgccgatg ccaccggcct 360
215 gtgggtctct gaagggaccc ccccccaatc ggactgcaa attctccggt ttgccccggg 420
216 atattataga aaattatttg tatgaataat gaaaataaaa cacacctcgt ggcaaaaaaa 480
217 aaaaaaaaaa a 491

```

220 &lt;210&gt; SEQ ID NO: 14

221 &lt;211&gt; LENGTH: 206

222 &lt;212&gt; TYPE: DNA

223 &lt;213&gt; ORGANISM: Artificial Sequence

225 &lt;220&gt; FEATURE:

226 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED

227 HUMAN

229 &lt;400&gt; SEQUENCE: 14

```

230 tttttttttt ttttttttgg gagtggtagg atgaaacaat ttggagaaga tagaagtttg 60
231 aagtggaaaa ctggaagaca gaagtacggg aaggcgaaga aaagaataga gaagataggg 120
232 aaattagaag ataaaaacat acttttagaa gaaaaaagat aaatttaaac ctgaaaagta 180
233 ggaagcagaa aaaaaaaaaa aaaaaa 206

```

236 &lt;210&gt; SEQ ID NO: 15

237 &lt;211&gt; LENGTH: 206

238 &lt;212&gt; TYPE: DNA

239 &lt;213&gt; ORGANISM: Artificial Sequence

241 &lt;220&gt; FEATURE:

242 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED

243 HUMAN

245 &lt;220&gt; FEATURE:

246 &lt;223&gt; OTHER INFORMATION: n at position 54 is unknown.

248 &lt;400&gt; SEQUENCE: 15

```

W--> 249 ttttctgtgg ggccatcact ttattaaggg gtcacttaga aggtgggccc cctgncaaac 60
250 cgcgggactg tgatcgggct ccagctactt caccaccccg ggccagcctg ctccaggggt 120
251 cccttcctgc tgagagcagg cgagaggcag tcaggctcat gaagcagcca ccgggttttg 180
252 ctcaactgaa ggaatcacac tggaaa 206

```

255 &lt;210&gt; SEQ ID NO: 16

256 &lt;211&gt; LENGTH: 178

257 &lt;212&gt; TYPE: DNA

258 &lt;213&gt; ORGANISM: Artificial Sequence

260 &lt;220&gt; FEATURE:

261 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED

262 HUMAN

264 &lt;400&gt; SEQUENCE: 16

```

265 tttttttttt ttttttttct gtgtccactg gagagcttga gtcacactc aaagatcaga 60
266 ggacctacag agagggctct ttggtttgag gaccatggct tacctttcct gcctttgacc 120
267 catcacaccc catttctcc tctttccctc tccccgctgc caaaaaaaaa aaaaaaaa 178

```

270 &lt;210&gt; SEQ ID NO: 17

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,031

DATE: 08/06/2001

TIME: 15:32:37

Input Set : A:\Gilad2b1.app

Output Set: N:\CRF3\08062001\I833031.raw

```

271 <211> LENGTH: 127
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
277     HUMAN
279 <220> FEATURE:
280 <223> OTHER INFORMATION: n at positions (98) and 112 are unknown.
282 <400> SEQUENCE: 17
283 gaattc gatg cgtattctgt ggcccgccat ctgcgcaggg tgggtgtatt ctgccattta 60
W--> 284 cacacgtcgt tctaattaaa aagcgaatna tactccaaaa aaaaaaaaaa ahgcggccgt 120
285 tgaattc 127
288 <210> SEQ ID NO: 18
289 <211> LENGTH: 115
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
295     HUMAN
297 <400> SEQUENCE: 18
298 gaattcagcg gccgcttttt tttttttttt tcttcgaagt gtttacccca gtgtttgaaa 60
299 gggattccag atggtcaaata aaaaaaaatg ttcctaaact tggatgatg aactc 115
302 <210> SEQ ID NO: 19
303 <211> LENGTH: 204
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
309     HUMAN
311 <220> FEATURE:
312 <223> OTHER INFORMATION: n at position 28 is unknown.
314 <400> SEQUENCE: 19
W--> 315 gaattcaggg ccgttctggt tctctcttnc tccccgccct ccctcaccac cagtgggaacc 60
316 ttcacgcagt tccacaaacc tggatttttt atgtacaacc ctgaccgtgg ccgtttgcta 120
317 tattcctttt tctatgaaat aatgtgaatg ataataaaac agctttgact tgaaaaaaaa 180
318 aaaaaaaaaa cggccgctga attc 204
321 <210> SEQ ID NO: 20
322 <211> LENGTH: 109
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR AMPLIFIED
328     HUMAN
330 <400> SEQUENCE: 20
331 gaattccctc cccctccttg tgccttcttt gtatataggc ttctcacggc gaccaataaa 60
332 cagctcccag tttgatgca aaaaaaaaaa aaaagcggcc gctgaattc 109
335 <210> SEQ ID NO: 21
336 <211> LENGTH: 191
337 <212> TYPE: DNA

```

*not ok 6 of 7*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/833,031

DATE: 08/06/2001

TIME: 15:32:38

Input Set : A:\Gilad2b1.app

Output Set: N:\CRF3\08062001\I833031.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:35 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:35 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:188 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:188 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:190 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:192 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:192 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:193 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:193 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:194 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:194 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:195 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:195 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:284 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:315 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:315 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:397 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:457 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27  
L:457 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27  
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:461 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27  
L:461 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27  
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:462 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27  
L:462 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27  
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27